13. (New) A host cell comprising the recombinant expression vector of claim 8.--

## RESPONSE

### I. Restriction Requirement

The Examiner has determined that the original claims are directed to two separate and distinct inventions under 35 U.S.C. § 121, as follows:

Group I: Claims 1 (in part) and 2-4, said to be drawn to an isolated nucleic acid encoding the polypeptide comprising the amino acid sequence set forth in SEQ ID NOS:2 and 6, classified in class 435, subclass 69.1; and

Group II: Claims 1 (in part) and 5, said to be drawn to an isolated nucleic acid which encodes the polypeptide comprising the amino acid sequence set forth in SEQ ID NO:8, classified in class 435, subclass 69.1.

### II. Response to Restriction Requirement

In response to the Restriction Requirement, Applicants hereby confirm the election without traverse, made by Applicants' representative David Hibler during a telephone conference with the Examiner on September 16, 2002, to prosecute the claims of the Group I invention (claims 1 (in part) and 2-4), drawn to an isolated nucleic acid encoding the polypeptide comprising the amino acid sequence set forth in SEQ ID NOS:2 and 6, classified in class 435, subclass 69.1. Accordingly, claim 5 has been cancelled herein without prejudice and without disclaimer as being drawn to a non-elected invention.

Applicants note for the record that claim 1 as originally filed also claimed an isolated nucleic acid encoding the polypeptide comprising the amino acid sequence set forth in SEQ ID NO:4, which is not included in the current Restriction Requirement. Applicants assume that this aspect of the present invention was inadvertently left out of the current Restriction Requirement, and that the Examiner would consider an isolated nucleic acid encoding the polypeptide comprising the amino acid sequence set forth in SEQ ID NO:4 as a separate invention from the Group I and Group II inventions set forth above. Therefore, Applicants confirm for the record the election of the Group I invention as set forth above without traverse, which means that reference to SEQ ID NO:4 will be removed from claim 1 as directed to a non-elected invention.

Applicants reserve the right to refile claims to the non-elected inventions in one or more future

applications retaining the priority date of the present case and the earlier cited priority applications.

## III. Status of the Claims

Claim 5, representing the Group II invention, has been cancelled without prejudice and without disclaimer as being drawn to a non-elected invention. Claims 1 and 2 have been amended. New claims 6-13 have been added.

Claims 1-4 and 6-13 are therefore presently pending in the case. For the convenience of the Examiner, a clean copy of the pending claims is attached hereto as **Exhibit A**. In compliance with 37 C.F.R. § 1.121(c)(1)(ii), a marked up copy of the original claims is attached hereto as **Exhibit B**.

## IV. Support for the Amended and Newly Added Claims

Claim 1 has been amended to further clarify the claim, and to remove reference to the non-elected inventions. Support for this claim can be found throughout the specification as originally filed.

Claim 2 has been amended to recite that the stringent hybridization conditions are highly stringent hybridization conditions. Support for these claims can be found throughout the specification as originally filed, with particular support being found at least at page 4, lines 15-22.

Claim 6 has been added to specifically claim the circumstance wherein SEQ ID NO:2 is encoded by SEQ ID NO:1. Support for this claim can be found throughout the specification as originally filed, with specific support being found at least in Section 5.1.

Claim 7 has been added to specifically claim the circumstance wherein SEQ ID NO:6 is encoded by SEQ ID NO:5. Support for this claim can be found throughout the specification as originally filed, with specific support being found at least in Section 5.1.

Claims 8-12 have been added to specifically recite recombinant expression vectors comprising isolated nucleic acid molecules of the invention. Support for these claims can be found throughout the specification as originally filed, with particular support being found at least at page 13, lines 27-33.

Claim 13 has been added to specifically recite host cells comprising the recombinant expression vectors of claim 8. Support for this claim can be found throughout the specification as originally filed, with particular support being found at least from page 13, line 33 to page 14, line 6.

It will be understood that no new matter is included within the amended or newly added claims.

## V. Objection to Claim 1

The Action first objects to claim 1 due to the phrase "comprising at a nucleotide sequence" (emphasis added), correctly surmising that the word "at" was an inadvertent clerical error. Applicants have corrected the error, and respectfully request that the objection to claim 1 be withdrawn.

## VI. Rejection of Claims 1-4 Under 35 U.S.C. § 101

The Action first rejects claims 1-4 under 35 U.S.C. § 101, as allegedly lacking a patentable utility. Applicants respectfully traverse.

The present invention has a number of substantial and credible utilities, not the least of which is in diagnostic assays, as described in the specification, at least at page 8, line 3, and from page 10, line 27 through page 11, line 1. As described in the specification from page 16, line 25 through page 17, line 2, the present sequences define two coding single nucleotide polymorphisms - specifically, a G/C polymorphism at position 212 of SEQ ID NO:1, which can lead to a glycine or alanine residue at amino acid position 71 of SEQ ID NO:2, and an A/C polymorphism at position 219 of SEQ ID NO:1, which can lead to a lysine or asparagine residue at amino acid position 73 of SEQ ID NO:2. The Action states that because "the particular medical conditions that can be diagnosed using the claimed nucleic acid (*sic*) are not disclosed" (Action at page 6), the skilled artisan would not know how to perform diagnostic assays using the presently claimed nucleic acids. However, as such polymorphisms are the basis for diagnostic assays such as forensic analysis, which does **not** require the identification of a specific medical condition, and is undoubtedly a "real world" utility, the present sequences must in themselves be useful. It is important to note that the presence of more useful polymorphic markers for forensic analysis would not mean that the present sequences lack utility. As clearly set forth by the Federal Circuit in *Carl Zeiss Stiftung v. Renishaw PLC*, 20 USPQ2d 1101 (Fed. Cir. 1991):

> An invention need not be the best or only way to accomplish a certain result, and it need only be useful to some extent and in certain applications: "[T]he fact that an invention has only limited utility and is only operable in certain applications is not grounds for finding a lack of utility." *Envirotech Corp. v. Al George, Inc.*, 221 USPQ 473, 480 (Fed. Cir. 1984)

Just because other polymorphic sequences from the human genome have been described does not mean that the use of the presently described polymorphic markers for forensic analysis is not a specific utility.

As an additional example of the utility of the present nucleotide sequences, the specification

details on page 5, lines 24-26, that the present nucleotide sequences have utility in assessing gene expression patterns using high-throughput DNA chips. Such "DNA chips" clearly have utility, as evidenced by hundreds of issued U.S. Patents, as exemplified by U.S. Patent Nos. 5,445,934, 5,556,752, 5,744,305, 5,837,832, 6,156,501 and 6,261,776. As the present sequences are specific markers of the human genome (see below), and such specific markers are targets for the discovery of drugs that are associated with human disease, those of skill in the art would instantly recognize that the present nucleotide sequences would be an ideal, novel candidate for assessing gene expression using such DNA chips. Given the widespread utility of such "gene chip" methods using *public domain* gene sequence information, there can be little doubt that the use of the presently described *novel* sequences would have great utility in such DNA chip applications. Clearly, compositions that enhance the utility of such DNA chips, such as the presently claimed nucleotide sequences, must in themselves be useful.

Evidence of the "real world" substantial utility of the present invention is further provided by the fact that there is an entire industry established based on the use of gene sequences or fragments thereof in a gene chip format. Perhaps the most notable gene chip company is Affymetrix. However, there are many companies which have, at one time or another, concentrated on the use of gene sequences or fragments, in gene chip and non-gene chip formats, for example: Gene Logic, ABI-Perkin-Elmer, HySeq and Incyte. In addition, two such companies (Agilent acquired by American Home Products and Rosetta acquired by Merck) were viewed to have such "real world" value that they were acquired by large pharmaceutical companies for significant sums of money. The "real world" substantial industrial utility of gene sequences or fragments would, therefore, appear to be widespread and well established. Clearly, persons of skill in the art, as well as venture capitalists and investors, readily recognize the utility, both scientific and commercial, of genomic data in general, and specifically human genomic data. Billions of dollars have been invested in the human genome project, resulting in useful genomic data (see, *e.g.*, Venter *et al.*, 2001, Science *291*:1304). The results have been a stunning success as the utility of human genomic data has been widely recognized as a great gift to humanity (see, *e.g.*, Jasny and Kennedy, 2001, Science *291*:1153). Clearly, the usefulness of human genomic data, such as the presently claimed nucleic acid molecules, is substantial and credible (worthy of billions of dollars and the creation of numerous companies focused on such information) and well-established (the utility of human genomic information has been clearly understood for many years).

Although Applicants need only make one credible assertion of utility to meet the requirements of 35 U.S.C. § 101 (*Raytheon v. Roper*, 220 USPQ 592 (Fed. Cir. 1983); *In re Gottlieb*, 140

USPQ 665 (CCPA 1964); *In re Malachowski*, 189 USPQ 432 (CCPA 1976); *Hoffman v. Klaus*, 9 USPQ2d 1657 (Bd. Pat. App. & Inter. 1988)), as a further example of the utility of the presently claimed polynucleotide, as described in the specification at least at page 2, lines 29-32, the present nucleotide sequences have a specific utility in "identification of coding sequence" and "mapping a unique gene to a particular chromosome". This is evidenced by the fact that SEQ ID NO:1 can be used to map the 5 coding exons on chromosome 17 (present within two independent chromosome 17 clones; Genbank Accession Numbers AC087644 and AC090685; alignments and the first page from the Genbank reports are presented in **Exhibit C**). Clearly, the present polynucleotide provides exquisite specificity in localizing the specific region of human chromosome 17 that contains the gene encoding the given polynucleotide, a utility not shared by virtually any other nucleic acid sequences. In fact, it is this specificity that makes this particular sequence so useful. Early gene mapping techniques relied on methods such as Giemsa staining to identify regions of chromosomes. However, such techniques produced genetic maps with a resolution of only 5 to 10 megabases, far too low to be of much help in identifying specific genes involved in disease. The skilled artisan readily appreciates the significant benefit afforded by markers that map a specific locus of the human genome, such as the present nucleic acid sequence.

Applicants respectfully remind the Examiner that only a minor percentage (2-4%) of the genome actually encodes exons, which in-turn encode amino acid sequences. The presently claimed polynucleotide sequence provides biologically validated empirical data (*e.g.*, showing which sequences are transcribed, spliced, and polyadenylated) that *specifically* define that portion of the corresponding genomic locus that actually encodes exon sequence, as described above. Equally significant is that the claimed polynucleotide sequence defines how the encoded exons are actually spliced together to produce an active transcript (*i.e.*, the described sequences are useful for functionally defining exon splice-junctions). The specification details that "sequences derived from regions adjacent to the intron/exon boundaries of the human gene can be used to design primers for use in amplification assays to detect mutations within the exons, introns, splice sites (*e.g.*, splice acceptor and/or donor sites), *etc.*, that can be used in diagnostics and pharmacogenomics" (specification at page 11, lines 1-6). Applicants respectfully submit that the practical scientific value of biologically validated, expressed, spliced, and polyadenylated mRNA sequences is readily apparent to those skilled in the relevant biological and biochemical arts. For further evidence in support of the Applicants' position, the Examiner is requested to review, for example, section 3 of Venter *et al.* (*supra at* pp. 1317-1321,

including Fig. 11 at pp.1324-1325), which demonstrates the significance of expressed sequence information in the structural analysis of genomic data. The presently claimed polynucleotide sequence defines a biologically validated sequence that provides a unique and specific resource for mapping the genome essentially as described in the Venter *et al.* article. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

Rather, as set forth by the Federal Circuit, "(t)he threshold of utility is not high: An invention is 'useful' under section 101 if it is capable of providing some identifiable benefit." *Juicy Whip Inc. v. Orange Bang Inc.*, 51 USPQ2d 1700 (Fed. Cir. 1999) (citing *Brenner v. Manson*, 383 U.S. 519, 534 (1966)). Additionally, the Federal Circuit has stated that "(t)o violate § 101 the claimed device must be totally incapable of achieving a useful result." *Brooktree Corp. v. Advanced Micro Devices, Inc.*, 977 F.2d 1555, 1571 (Fed. Cir. 1992), emphasis added. *Cross v. Iizuka* (224 USPQ 739 (Fed. Cir. 1985); "*Cross*") states "any utility of the claimed compounds is sufficient to satisfy 35 U.S.C. § 101". *Cross* at 748, emphasis added. Indeed, the Federal Circuit recently emphatically confirmed that "anything under the sun that is made by man" is patentable *(State Street Bank & Trust Co. v. Signature Financial Group Inc.*, 47 USPQ2d 1596, 1600 (Fed. Cir. 1998), citing the U.S. Supreme Court's decision in *Diamond vs. Chakrabarty*, 206 USPQ 193 (S.Ct. 1980)).

The Action states that the present sequence lacks utility because any "specific diseases which (*sic*) can be treated or diagnosed using the NHP protein encoded by the claimed nucleic acids" are not disclosed (Action at page 6). However, this is not the standard required for utility under 35 U.S.C. § 101. In *In re Brana*, (34 USPQ2d 1436 (Fed. Cir. 1995), "*Brana*"), the Federal Circuit admonished the P.T.O. for confusing "the requirements under the law for obtaining a patent with the requirements for obtaining government approval to market a particular drug for human consumption". *Brana* at 1442. The Federal Circuit went on to state:

> At issue in this case is an important question of the legal constraints on patent office examination practice and policy. The question is, with regard to pharmaceutical inventions, what must the applicant provide regarding the practical utility or usefulness of the invention for which patent protection is sought. This is not a new issue; it is one which we would have thought had been settled by case law years ago.

*Brana* at 1439, emphasis added. The choice of the phrase "utility or usefulness" in the foregoing quotation is highly pertinent. The Federal Circuit is evidently using "utility" to refer to rejections under 35 U.S.C. § 101, and is using "usefulness" to refer to rejections under 35 U.S.C. § 112, first paragraph. This is made evident in the continuing text in *Brana*, which explains the correlation between 35 U.S.C. §§ 101 and 112, first paragraph. The Federal Circuit concluded:

> FDA approval, however, is not a prerequisite for finding a compound useful within the meaning of the patent laws. Usefulness in patent law, and in particular in the context of pharmaceutical inventions, necessarily includes the expectation of further research and development. The stage at which an invention in this field becomes useful is well before it is ready to be administered to humans. Were we to require Phase II testing in order to prove utility, the associated costs would prevent many companies from obtaining patent protection on promising new inventions, thereby eliminating an incentive to pursue, through research and development, potential cures in many crucial areas such as the treatment of cancer.

*Brana* at 1442-1443, citations omitted. The Action states that the claimed sequences lack utility because "basic research" (Action at page 7) would be required in certain aspects of the invention. Even if, *arguendo*, further research might be required in certain aspects of the present invention, this does not preclude a finding that the invention has utility, as set forth by the Federal Circuit's holding in *Brana*, which clearly states, as highlighted in the quote above, that "pharmaceutical inventions, necessarily includes the expectation of <u>further research and development</u>" (*Brana* at 1442-1443, emphasis added). In assessing the question of whether undue experimentation would be required in order to practice the claimed invention, the key term is "undue", not "experimentation". *In re Angstadt and Griffin*, 190 USPQ 214 (CCPA 1976). The need for some experimentation does not render the claimed invention unpatentable. Indeed, a considerable amount of experimentation may be permissible if such experimentation is routinely practiced in the art. *In re Angstadt and Griffin*, *supra*; *Amgen, Inc. v. Chugai Pharmaceutical Co., Ltd.*, 18 USPQ2d 1016 (Fed. Cir. 1991). As a matter of law, it is well settled that a patent need not disclose what is well known in the art. *In re Wands*, 8 USPQ 2d 1400 (Fed. Cir. 1988).

Finally, the requirements set forth in the Action for compliance with 35 U.S.C. § 101 do not comply with the requirements set forth by the Patent and Trademark Office ("the PTO") <u>itself</u> for compliance with 35 U.S.C. § 101. While Applicants are well aware of the new Utility Guidelines set forth by the USPTO, Applicants respectfully point out that the current rules and regulations regarding the examination of patent applications is and always has been the patent laws as set forth in 35 U.S.C. and the patent rules as set forth in 37 C.F.R., not the Manual of Patent Examination Procedure or particular guidelines for patent examination set forth by the USPTO. Furthermore, it is the job of the judiciary, <u>not</u> the USPTO, to interpret these laws and rules. Applicants are unaware of any significant recent changes in either 35 U.S.C. § 101, or in the interpretation of 35 U.S.C. § 101 by the Supreme Court or the Federal Circuit that is in keeping with the new Utility Guidelines set forth by the USPTO. This is underscored by numerous patents that have been issued over the years that claim nucleic acid

fragments that do not comply with the new Utility Guidelines. As examples of such issued U.S. Patents, the Examiner is invited to review U.S. Patent Nos. 5,817,479, 5,654,173, and 5,552,281 (each of which claims short polynucleotides), and recently issued U.S. Patent No. 6,340,583 (which includes no working examples), none of which contain examples of the "real-world" utilities that the Examiner seems to be requiring. As issued U.S. Patents are presumed to meet all of the requirements for patentability, including 35 U.S.C. §§ 101 and 112, first paragraph (see Section VII, below), Applicants submit that the present polynucleotides must also meet the requirements of 35 U.S.C. § 101. While Applicants understand that each application is examined on its own merits, Applicants are unaware of any changes to 35 U.S.C. § 101, or in the interpretation of 35 U.S.C. § 101 by the Supreme Court or the Federal Circuit, since the issuance of these patents that render the subject matter claimed in these patents, which is similar to the subject matter in question in the present application, as suddenly non-statutory or failing to meet the requirements of 35 U.S.C. § 101. Thus, holding Applicants to a different standard of utility would be arbitrary and capricious, and, like other clear violations of due process, cannot stand.

For each of the foregoing reasons, Applicants submit that as the presently claimed nucleic acid molecules have been shown to have a substantial, specific, credible and well-established utility, the rejection of claims 1-4 under 35 U.S.C. § 101 has been overcome, and request that the rejection be withdrawn.

## VII. Rejection of Claims 1-4 Under 35 U.S.C. § 112, First Paragraph

The Action next rejects claims 1-4 under 35 U.S.C. § 112, first paragraph, since allegedly one skilled in the art would not know how to use the invention, as the invention allegedly is not supported by a specific, substantial, and credible utility or a well-established utility. Applicants respectfully traverse.

Applicants submit that as claims 1-4 have been shown to have "a specific, substantial, and credible utility", as detailed in section VI above, the present rejection of claims 1-4 under 35 U.S.C. § 112, first paragraph, cannot stand.

Applicants therefore request that the rejection of claims 1-4 under 35 U.S.C. § 112, first paragraph, be withdrawn.

## VIII. Rejection of Claim 2 Under 35 U.S.C. § 112, Second Paragraph

The Action next rejects claim 2 under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite for failing to particularly point out and distinctly claim the invention.

The Action rejects claim 2 as allegedly indefinite based on the term "stringent hybridization conditions", because the specific hybridization and washing conditions are not recited in the claim. Applicants stress that "a claim need not 'describe' the invention, such description being the role of the disclosure". *Orthokinetics, Inc. v. Safety Travel Chairs, Inc.*, 1 USPQ2d 1081, 1088 (Fed. Cir. 1986). However, while Applicants submit that the term is sufficiently definite, as a number of stringent hybridization conditions are defined in the specification and would be known to those of skill in the art, solely in order to progress the case more rapidly toward allowance the claim has been revised to specifically recite "highly" stringent hybridization conditions. As the specification provides specific teaching regarding "highly stringent hybridization conditions", at least at page 4, lines 15-22, Applicants submit that revised claim 2 even more clearly meets the requirements of 35 U.S.C. § 112, second paragraph. Applicants therefore request withdrawal of this rejection.

## IX. Conclusion

The present document is a full and complete response to the Action. In conclusion, Applicants submit that, in light of the foregoing remarks, the present case is in condition for allowance, and such favorable action is respectfully requested. Should Examiner Hamud have any questions or comments, or believe that certain amendments of the claims might serve to improve their clarity, a telephone call to the undersigned Applicants' representative is earnestly solicited.

Respectfully submitted,

February 21, 2003
Date

David W. Hibler Reg. No. 41,071
Agent for Applicants

LEXICON GENETICS INCORPORATED
8800 Technology Forest Place
The Woodlands, TX 77381
(281) 863-3399

**Exhibit B**

**Marked Up Version of Amended Claims in U.S. Patent Application Ser. No. 09/863,823**

1. (Amended) An isolated nucleic acid molecule comprising [at] a nucleotide sequence encoding [an] the amino acid sequence [drawn from the group consisting] of SEQ ID NOS:2[, 4,] or 6 [and 8].

2. (Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:

(a ) encodes the amino acid sequence shown in SEQ ID NO:2; and

(b) hybridizes under highly stringent conditions to the nucleotide sequence of SEQ ID NO:1 or the complement thereof.

3. An isolated nucleic acid molecule comprising a nucleotide sequence encoding the amino acid sequence shown in SEQ ID NO:2.

4. An isolated nucleic acid molecule comprising a nucleotide sequence encoding the amino acid sequence shown in SEQ ID NO:6.

5. (Cancelled) An isolated nucleic acid molecule comprising a nucleotide sequence encoding the amino acid sequence shown in SEQ ID NO:8.

6. (New) The isolated nucleic acid molecule of claim 3, wherein said nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO:1.

7. (New) The isolated nucleic acid molecule of claim 4, wherein said nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO:5.

8. (New) A recombinant expression vector comprising the isolated nucleic acid molecule of claim 1.

9. (New) The recombinant expression vector of claim 8, wherein the isolated nucleic acid

molecule encodes the amino acid sequence shown in SEQ ID NO:2.

10. (New) The recombinant expression vector of claim 9, wherein the isolated nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO:1.

11. (New) The recombinant expression vector of claim 8, wherein the isolated nucleic acid molecule encodes the amino acid sequence shown in SEQ ID NO:6.

12. (New) The recombinant expression vector of claim 11, wherein the isolated nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO:5.

13. (New) A host cell comprising the recombinant expression vector of claim 8.

**Query=** SEQ ID NO:1
(789 letters)

Sequences producing significant alignments:

| | Score (bits) | E Value |
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Score = 554 bits (279), Expect = e-155
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 Strand = Plus / Minus


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 Strand = Plus / Minus


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          Length = 171140

 Score =  554 bits (279), Expect = e-155
 Identities = 279/279 (100%)
 Strand = Plus / Minus


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Sbjct: 56670 caatcaccaaagtcgagaagcctgacaacggaacctacagttgtattgcaaagtcatctc 56611


Query: 602   tgaaaacggagagcttggactttcacctgattgttaaag 640
              |||||||||||||||||||||||||||||||||||||
Sbjct: 56610 tgaaaacggagagcttggactttcacctgattgttaaag 56572


 Score =  547 bits (275), Expect = e-153
 Identities = 277/279 (99%)
 Strand = Plus / Minus


Query: 83    gttctgttttaactgtgaatggtaaaactgagaactatatcctggatactacacctggct 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61293 gttctgttttaactgtgaatggtaaaactgagaactatatcctggatactacacctggct 61234


Query: 143   cccaagcatctctgatatgtgctgttcaaaaccacaccagagaggaagaactgctctggt 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61233 cccaagcatctctgatatgtgctgttcaaaaccacaccagagaggaagaactgctctggt 61174


Query: 203   accgagaggaggggagagtggatttgaaatctgsaaacaamatcaattccagctctgtct 262
              |||||||||||||||||||||||||||||| |||||| ||||||||||||||||||||
Sbjct: 61173 accgagaggaggggagagtggatttgaaatctggaaacaaaatcaattccagctctgtct 61114
```

```
Query: 263   gtgtctcttccatcagtgaaaatgacaacggaatcagctttacctgcaggctggggaggg 322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61113 gtgtctcttccatcagtgaaaatgacaacggaatcagctttacctgcaggctggggaggg 61054


Query: 323   atcagtccgtgtccgtttcggtggtgctgaatgttactt 361
             |||||||||||||||||||||||||||||||||||||
Sbjct: 61053 atcagtccgtgtccgtttcggtggtgctgaatgttactt 61015
```

Score = 211 bits (106), Expect = 7e-52
Identities = 106/106 (100%)
Strand = Plus / Minus

```
Query: 639   agataaaactgtgggtgtaccaatagagcccattattgctgcatgtgttgtgatctttct 698
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50671 agataaaactgtgggtgtaccaatagagcccattattgctgcatgtgttgtgatctttct 50612


Query: 699   gacattgtgctttggactgattgctagaagaaagaaaataatgaag 744
             |||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50611 gacattgtgctttggactgattgctagaagaaagaaaataatgaag 50566
```

Score = 163 bits (82), Expect = 2e-37
Identities = 83/84 (98%)
Strand = Plus / Minus

```
Query: 1     atggcatggaagagcagtgtcataatgcaratgggaagatttcttctcttagtaatttta 60
             |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct: 63900 atggcatggaagagcagtgtcataatgcaaatgggaagatttcttctcttagtaatttta 63841


Query: 61    tttctgccacgtgagatgacaagt 84
             |||||||||||||||||||||||
Sbjct: 63840 tttctgccacgtgagatgacaagt 63817
```

Score = 85.9 bits (43), Expect = 3e-14
Identities = 43/43 (100%)
Strand = Plus / Minus

```
Query: 743   agctctgcatgaaggataaagaccctcacagtgaaacagctct 785
             |||||||||||||||||||||||||||||||||||||||||||
Sbjct: 48991 agctctgcatgaaggataaagaccctcacagtgaaacagctct 48949
```

**1:** AC087644. Homo sapiens chro...[gi:22655825] Links

```
LOCUS       AC087644               102286 bp    DNA     linear   PRI 03-SEP-2002
DEFINITION  Homo sapiens chromosome 17, clone RP11-403E9, complete sequence.
ACCESSION   AC087644
VERSION     AC087644.8  GI:22655825
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 102286)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-403E9
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 102286)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A.,
            Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
            Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
            Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J.,
            Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
            Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T.,
            Lehoczky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P.,
            Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
            McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
            Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
            O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
            Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
            Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
            Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
            Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
            Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
            Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-2001) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 102286)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
            Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
            Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
            Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
```

1: AC090685. Homo sapiens chro...[gi:18698797]



LOCUS AC090685 171140 bp DNA linear PRI 17-FEB-2002
DEFINITION Homo sapiens chromosome 17, clone RP11-252O24, complete sequence.
ACCESSION AC090685
VERSION AC090685.8 GI:18698797
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 171140)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 17, clone RP11-252O24
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 171140)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (08-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 171140)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,